

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 101732,706

Source: _____

Date Processed by STIC: _____

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 02/16/2005

PATENT APPLICATION: US/10/732,706

TIME: 14:18:35

Input Set : N:\CrF3\RULE60\10732706.raw.txt

Output Set: N:\CRF4\02162005\J732706.raw

```

1 <110> APPLICANT: Ikezu, Tsuneya
2      Leisman, Gary
3      Carlson, Kimberly A.
4      Gendelman, Howard E.
5      University of Nebraska Medical Center
6 <120> TITLE OF INVENTION: Methods and Compositions for the
7      Treatment of Human Immunodeficiency Virus Infection
8 <130> FILE REFERENCE: UNMC 63156
9 <140> CURRENT APPLICATION NUMBER: US/10/732,706
10 <141> CURRENT FILING DATE: 2003-12-10
11 <150> PRIOR APPLICATION NUMBER: US/09/828,648
12 <151> PRIOR FILING DATE: 2001-04-06
13 <150> PRIOR APPLICATION NUMBER: 60/246,331
14 <151> PRIOR FILING DATE: 2000-11-06
15 <160> NUMBER OF SEQ ID NOS: 14
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 3734
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1
23      gctaagccta tgctgcttac tggacgctga agtgattggg aatattagca gtgggggttc      60
24      tgtaggggtca ggaaggggag gctggctttg ggggagtgat gaggggcttg ttgggggttg      120
25      ggggtgcgtga taaagggatt tctcggctga agacgaggct gtgaggcttc tgcagaaccc      180
26      ccaggctcagg ccacatcatt gaggtgcag gatctctctt catagcccag tacgactctc      240
27      cgccgtgtcc ctggttggaa aatccaaaca cctatccagc ttctggctcc tgggaaaagt      300
28      ggagttgtca gcaagagaga ccgagagtag aagcccagag tggagatgcc tgctgatgtg      360
29      aatttatccc agaagcctca ggtcctgggt ccagagaagc aggatggatc ttgcgaggca      420
30      tcagtgtcat ttgaggacgt gaccgtggac ttcagcaggg aggagtggca gcaactggac      480
31      cctgcccaga gatgcctgta ccgggatgtg atgctggagc tctatagcca tctcttcgca      540
32      gtgggggtatc acattcccaa ccagaggtc atcttcagaa tgctaaaaga aaaggagccg      600
33      cgtgtggagg aggtgaagt ctacatcag aggtgtcaag aaaggagtt tgggcttgaa      660
34      atcccacaaa aggagatttc taagaaagct tcatctcaaa aggatatggt aggtgagttc      720
35      acaagagatg gttcatggtg ttccatttta gaagaactga ggctggatgc tgaccgcaca      780
36      aagaaagatg agcaaaatca aattcaaccc atgagtcaca gtgctttctt caacaagaaa      840
37      acattgaaca cagaaagcaa ttgtgaatat aaggaccctg ggaaaatgat tcgcacgagg      900
38      cccaccttg cttcttcaca gaaacaacct cagaaatgtt gcttattttac agaaagtttg      960
39      aagctgaacc tagaagtga cggtcagaat gaaagcaatg acacagaaca gcttgatgac      1020
40      gttgttgggt ctggtcagct attcagccat agctcttctg atgcttcag caagaatatt      1080
41      catacaggag agacattttg caaaggtaac cagtgtagaa aagtctgtgg ccataaacag      1140
42      tcaactcaagc aacatcaaat tcatactcag aagaaaccag atggatgttc tgaatgtggg      1200
43      gggagcttca ccagaaagtc acacctctt gcccaacaga gaattcatag tgtaggaaac      1260
44      ctccatgaat gtggcaaatg tggaaaagcc ttcatgccac aactaaaact cagtgtatat      1320

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45	ctgacagatc	atacaggtga	tataccctgt	atatgcaagg	aatgtgggaa	ggtcttttatt	1380
46	cagagatcag	aattgcttac	gcaccagaaa	acacacacta	gaaagaagcc	ctataaatgc	1440
47	catgactgtg	gaaaagcctt	tttccagatg	ttatctctct	tcagacatca	gagaactcac	1500
48	agtagagaaa	aactctatga	atgcagtga	tgtggcaaag	gcttctccca	aaactcaacc	1560
49	ctcattatac	atcagaaaat	tcatactggt	gagagacagt	atgcatgcag	tgaatgtggg	1620
50	aaagccttta	cccagaagtc	aacactcagc	ttgcaccaga	gaatccactc	agggcagaag	1680
51	tcctatgtgt	gtatcgaatg	cgggcaggcc	ttcatccaga	aggcacacct	gattgtccat	1740
52	caaagaagcc	acacaggaga	aaaaccttat	cagtgccaca	actgtgggaa	atccttcatt	1800
53	tccaagtcac	agcttgatat	acatcatcga	attcatacag	gggagaaacc	ttatgaatgc	1860
54	agtgactgtg	gaaaaacctt	cacccaaaag	tcacacctga	atataacca	gaaaattcat	1920
55	actggagaaa	gacaccatgt	atgcagtga	tgcgggaaag	ccttcaacca	gaagtcaata	1980
56	ctcagcatgc	atcagagaat	tcacaccgga	gagaagcctt	acaaatgcag	tgaatgtggg	2040
57	aaagccttca	cttctaagtc	tcaattcaaa	gagcatcagc	gaattcacac	gggtgagaaa	2100
58	ccctatgtgt	gcaatgaatg	tgggaaggcc	ttcaacggca	ggtcaaattt	ccataaacat	2160
59	caaataactc	acactagaga	gaggcctttt	gtctgttaca	aatgtgggaa	ggcttttgtc	2220
60	cagaaatcag	agttgattac	ccatcaaaga	actcacatgg	gagagaaacc	ctatgaatgc	2280
61	cttgactgtg	ggaaatcggt	cagtaagaaa	ccacaactca	agggtgatca	gcgaattcac	2340
62	acgggagaaa	gaccttatgt	gtgttctgaa	tgtggaaagg	ccttcaacaa	cagggtcaaac	2400
63	ttcaataaac	accaaacaac	tcataccaga	gacaaatcct	acaaatgcag	ttattctgtg	2460
64	aaaggcttta	ccaagcaatg	aattcctagt	gcatacagcat	attcataaat	gaaatatact	2520
65	ccgagtttct	tgaagaagag	aacatcttct	cagaatcagg	tctaattata	tgttattgaa	2580
66	ttcatgcttc	agaaaaactc	tagggatgca	ctgcatgtgt	gaacacatga	taaaaaagtc	2640
67	atgcttttatt	ttagttaggg	caattacaga	gaaaagagta	agcagaaatg	tccttctgag	2700
68	tactggcctc	attaaggatt	ataaattttc	tccccgggaa	gaaaccctga	ctaacgcatt	2760
69	gagaaaagcc	tttctgtaaa	gaatggtaca	agacagggtg	ttactcgatt	atztatagta	2820
70	aaatatgtgg	gaaattatat	caatgataac	cctgttttatt	gtgggatatac	aatattttta	2880
71	aagtgccaac	acagtcatga	taggacaata	ttttatgtgt	gtgtgtgcgc	cttatgtata	2940
72	taagcatata	tataatatat	aagcatatta	ttatatacag	gttgagtatac	ccttctccaa	3000
73	aatgcctggg	atcagaagca	ttttggattt	cagatactta	cagatttttg	aatattttgca	3060
74	ttatatttat	tggttgagca	tcctaatct	gaaaatccaa	gattaaatgc	tccaattagc	3120
75	atttcctttg	agcgtcatgt	tagagttcaa	aaagtttcag	attttgggtt	ttcagattag	3180
76	gaatacccaa	cctgtatgta	cgtatatttc	tgtatctatg	tatgtatata	tatgcatatg	3240
77	cagacatatg	tatatggtct	ggtcagcata	tgtgtatgta	tgcgtatgta	tgtatgtatg	3300
78	tatgccctca	gtgcagtggg	gtttgctgca	gaattcactg	catagcagga	gatgtaagca	3360
79	gatgagttat	tttttaagag	aatctaactc	aattgttttt	ataaaaatta	ttcctattg	3420
80	aatattttata	taatgaggtt	gtatcaacaa	tgattaactc	ctttattata	catacacatg	3480
81	aatgtgcatt	tttggtaaat	gcataaatga	gattctataa	tgtttactga	tctttatatt	3540
82	acagattttc	tcttctttta	ggattagctc	agcttgcccc	ccctttccat	ctccaccatc	3600
83	tatagtgagc	ctctccataa	ttagtgccaa	ccattagtct	cgttcataatt	tttacaccag	3660
84	gagtcaacaa	actgtgccat	tggccaaata	tggcctccca	actgtttttt	taaaataaag	3720
85	ttttattgga	acac					3734
87	<210>	SEQ ID NO: 2					
88	<211>	LENGTH: 711					
89	<212>	TYPE: PRT					
90	<213>	ORGANISM: Homo sapiens					
91	<400>	SEQUENCE: 2					
92		Met Pro Ala Asp Val Asn Leu Ser Gln Lys Pro Gln Val Leu Gly Pro					
93		1 5 10 15					
94		Glu Lys Gln Asp Gly Ser Cys Glu Ala Ser Val Ser Phe Glu Asp Val					

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```

95          20          25          30
96  Thr Val Asp Phe Ser Arg Glu Glu Trp Gln Gln Leu Asp Pro Ala Gln
97          35          40          45
98  Arg Cys Leu Tyr Arg Asp Val Met Leu Glu Leu Tyr Ser His Leu Phe
99          50          55          60
100  Ala Val Gly Tyr His Ile Pro Asn Pro Glu Val Ile Phe Arg Met Leu
101          65          70          75          80
102  Lys Glu Lys Glu Pro Arg Val Glu Glu Ala Glu Val Ser His Gln Arg
103          85          90          95
104  Cys Gln Glu Arg Glu Phe Gly Leu Glu Ile Pro Gln Lys Glu Ile Ser
105          100          105          110
106  Lys Lys Ala Ser Phe Gln Lys Asp Met Val Gly Glu Phe Thr Arg Asp
107          115          120          125
108  Gly Ser Trp Cys Ser Ile Leu Glu Glu Leu Arg Leu Asp Ala Asp Arg
109          130          135          140
110  Thr Lys Lys Asp Glu Gln Asn Gln Ile Gln Pro Met Ser His Ser Ala
111          145          150          155          160
112  Phe Phe Asn Lys Lys Thr Leu Asn Thr Glu Ser Asn Cys Glu Tyr Lys
113          165          170          175
114  Asp Pro Gly Lys Met Ile Arg Thr Arg Pro His Leu Ala Ser Ser Gln
115          180          185          190
116  Lys Gln Pro Gln Lys Cys Cys Leu Phe Thr Glu Ser Leu Lys Leu Asn
117          195          200          205
118  Leu Glu Val Asn Gly Gln Asn Glu Ser Asn Asp Thr Glu Gln Leu Asp
119          210          215          220
120  Asp Val Val Gly Ser Gly Gln Leu Phe Ser His Ser Ser Ser Asp Ala
121          225          230          235          240
122  Cys Ser Lys Asn Ile His Thr Gly Glu Thr Phe Cys Lys Gly Asn Gln
123          245          250          255
124  Cys Arg Lys Val Cys Gly His Lys Gln Ser Leu Lys Gln His Gln Ile
125          260          265          270
126  His Thr Gln Lys Lys Pro Asp Gly Cys Ser Glu Cys Gly Gly Ser Phe
127          275          280          285
128  Thr Gln Lys Ser His Leu Phe Ala Gln Gln Arg Ile His Ser Val Gly
129          290          295          300
130  Asn Leu His Glu Cys Gly Lys Cys Gly Lys Ala Phe Met Pro Gln Leu
131          305          310          315          320
132  Lys Leu Ser Val Tyr Leu Thr Asp His Thr Gly Asp Ile Pro Cys Ile
133          325          330          335
134  Cys Lys Glu Cys Gly Lys Val Phe Ile Gln Arg Ser Glu Leu Leu Thr
135          340          345          350
136  His Gln Lys Thr His Thr Arg Lys Lys Pro Tyr Lys Cys His Asp Cys
137          355          360          365
138  Gly Lys Ala Phe Phe Gln Met Leu Ser Leu Phe Arg His Gln Arg Thr
139          370          375          380
140  His Ser Arg Glu Lys Leu Tyr Glu Cys Ser Glu Cys Gly Lys Gly Phe
141          385          390          395          400
142  Ser Gln Asn Ser Thr Leu Ile Ile His Gln Lys Ile His Thr Gly Glu
143          405          410          415

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```

144   Arg Gln Tyr Ala Cys Ser Glu Cys Gly Lys Ala Phe Thr Gln Lys Ser
145           420                      425                      430
146   Thr Leu Ser Leu His Gln Arg Ile His Ser Gly Gln Lys Ser Tyr Val
147           435                      440                      445
148   Cys Ile Glu Cys Gly Gln Ala Phe Ile Gln Lys Ala His Leu Ile Val
149           450                      455                      460
150   His Gln Arg Ser His Thr Gly Glu Lys Pro Tyr Gln Cys His Asn Cys
151           465                      470                      475                      480
152   Gly Lys Ser Phe Ile Ser Lys Ser Gln Leu Asp Ile His His Arg Ile
153           485                      490                      495
154   His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Asp Cys Gly Lys Thr Phe
155           500                      505                      510
156   Thr Gln Lys Ser His Leu Asn Ile His Gln Lys Ile His Thr Gly Glu
157           515                      520                      525
158   Arg His His Val Cys Ser Glu Cys Gly Lys Ala Phe Asn Gln Lys Ser
159           530                      535                      540
160   Ile Leu Ser Met His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys
161           545                      550                      555                      560
162   Cys Ser Glu Cys Gly Lys Ala Phe Thr Ser Lys Ser Gln Phe Lys Glu
163           565                      570                      575
164   His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Val Cys Thr Glu Cys
165           580                      585                      590
166   Gly Lys Ala Phe Asn Gly Arg Ser Asn Phe His Lys His Gln Ile Thr
167           595                      600                      605
168   His Thr Arg Glu Arg Pro Phe Val Cys Tyr Lys Cys Gly Lys Ala Phe
169           610                      615                      620
170   Val Gln Lys Ser Glu Leu Ile Thr His Gln Arg Thr His Met Gly Glu
171           625                      630                      635                      640
172   Lys Pro Tyr Glu Cys Leu Asp Cys Gly Lys Ser Phe Ser Lys Lys Pro
173           645                      650                      655
174   Gln Leu Lys Val His Gln Arg Ile His Thr Gly Glu Arg Pro Tyr Val
175           660                      665                      670
176   Cys Ser Glu Cys Gly Lys Ala Phe Asn Asn Arg Ser Asn Phe Asn Lys
177           675                      680                      685
178   His Gln Thr Thr His Thr Arg Asp Lys Ser Tyr Lys Cys Ser Tyr Ser
179           690                      695                      700
180   Val Lys Gly Phe Thr Lys Gln
181           705                      710
183 <210> SEQ ID NO: 3
184 <211> LENGTH: 20
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Primer
189 <400> SEQUENCE: 3
190   gaaaatccaa acacctatcc
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 20
194 <212> TYPE: DNA

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20

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```

195 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Primer
198 <400> SEQUENCE: 4
199     aaggacattt ctgcttactc                                20
201 <210> SEQ ID NO: 5
202 <211> LENGTH: 19
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Primer
207 <400> SEQUENCE: 5
208     ggctgtcttc caataaaac                                19
210 <210> SEQ ID NO: 6
211 <211> LENGTH: 20
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Primer
216 <400> SEQUENCE: 6
217     gtgagcctct ccataattag                                20
219 <210> SEQ ID NO: 7
220 <211> LENGTH: 99
221 <212> TYPE: PRT
222 <213> ORGANISM: Homo sapiens
223 <400> SEQUENCE: 7
224     Met Ala Ala Asn Gly Asp Ser Pro Pro Trp Ser Pro Ala Leu Ala Ala
225         1             5             10             15
226     Glu Gly Arg Gly Ser Ser Cys Glu Ala Ser Val Ser Phe Glu Asp Val
227         20             25             30
228     Thr Val Asp Phe Ser Lys Glu Glu Trp Gln His Leu Asp Pro Ala Gln
229         35             40             45
230     Arg Arg Leu Tyr Trp Asp Val Thr Leu Glu Asn Tyr Ser His Leu Leu
231         50             55             60
232     Ser Val Gly Tyr Gln Ile Pro Lys Ser Glu Ala Ala Phe Lys Leu Glu
233         65             70             75             80
234     Gln Gly Glu Gly Pro Trp Met Leu Glu Gly Glu Ala Pro His Gln Ser
235         85             90             95
236     Cys Ser Gly
238 <210> SEQ ID NO: 8
239 <211> LENGTH: 84
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
242 <400> SEQUENCE: 8
243     Met Ala Pro Glu Gln Arg Glu Gly Ala Ser Gln Val Ser Val Thr Phe
244         1             5             10             15
245     Glu Asp Val Ala Val Leu Phe Thr Arg Asp Glu Trp Lys Lys Leu Asp
246         20             25             30
247     Leu Ser Gln Arg Ser Leu Tyr Arg Glu Val Met Leu Glu Asn Tyr Ser

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 2,9,13,15,16,20

Seq#:14; Xaa Pos. 7

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42

Seq#:1; Line(s) 43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62

Seq#:1; Line(s) 63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82

Seq#:1; Line(s) 83,84,85

Seq#:3; Line(s) 190

Seq#:4; Line(s) 199

Seq#:5; Line(s) 208

Seq#:6; Line(s) 217

VERIFICATION SUMMARY

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L:333 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13
L:349 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0